

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAACAGAAAACCTGTTAGAAATGTTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTATGCAATTG
CTACCATTTTATGTTTCGTTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTAGGACTTCTATTGTGGCAAACCTT
CCAGAAAAACAACCCTTTTGTGCTGCACATGTAAGTGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTTCCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACTTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIIFSITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSFSGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCCTTC
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
GATTTGGGTGGCTTTTCTTCATGCCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATCTGCTGATCCTGG
TTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAAACTAGGAGATCCCTTTCC
CATTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTTCTGGATTGGTGTCAACTGCCCATACACTTACATGTCTTACTTC
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
AACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACCTCAGCATCAGGAAGTGAAATCTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTTCTTGGTT
ACTTTTTCTCTATTTACTGTGTTTGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT
GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTTGGTCCCAACACATTTCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCCTCCAATGTCATTGTCCTG
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCCTT
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG
ATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAACAGGCACCA
GAGAAGCAAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTA
GATATAAGAGGGGGGAAAAATGGAACAGGGCCTGACATTTTATAAAACAAACAAAATGCTATGGTAGC
ATTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAGAGGCGGAGAGGAGCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTCCGTTTAAAGGTTACATGGAAGGTTATAGCTTTG
CCTTGAGATTGACTCATTAATAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
 AGAAGTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
 GTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT
 GTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
 AAGCTAAGGAGGCCGTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC
 TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGGATGGATTTCGTGGTCATCTCTAG
 GATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGA
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAATCGTGCATTCCAGAA
 ATTATCACCACCAAGATCCCATATTCAACACTCAAAGTGAACACAAACACAGAATTTATTGT
 CAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCCCTACTACTCCTC
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTTATG
 GAAACTAGCACCATGTCTACAGAACTGAACCAATTTGTTGAAAATAAGCAGCATTCAAGAATGA
 AGCTGCTGGGTTTGGAGGTGTCCCGACGGCTCTGCTAGTGTCTGCTCCTCTTCTTTGGTGTCTG
 CAGCTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAT
 CAGCAGAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAA
 TGAGGAATCAAAGAAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGC
 GATGCCGTGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT
 CATGCTCCTTACCCCTGCCCGAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCA
 CCGTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT
 GCCCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCT
 TTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGAAGGAC
 CTAACACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGGTGGGTTG
 AAAGCCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA
 GCTCTGAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAAGAGCAAAAGAAAT
 GGCAGAAAAGTTTAGCCCCGTGAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
 GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC
 ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTGAACACACACA
 CTTACTTTTCTGGTCTCTACCACTGCTGATTTTTCTCTAGGAAATATACTTTTACAAGTAACA
 AAAATAAAAACTCTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAACAAACATTTGCTGAATAGCTACTATATGTC
 AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTCACATAGTAG
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTGTATTTCTAGCTTATCTACTTCCAACTAAT
 TTTTATTTTGTGTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAAT
 TATTATTAACATACTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAAGTGCC
 ATTAACAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATT
 TGTGACAAAAAATTAAAGCATTAGAAAACCTT

FIGURE 6

MARCFSLVLLLSIWTTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKPVSRQFAAYCYN
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR
RKKLICVTEVEMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFPFNTKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGCCCGGC
GGCCTCCCGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCGGGGCGG
CGGCTGCGGGCGCAGAGCGGAGATCGAGCGGCTTGGGGCCACCCTGCTGTGCTGTGCTGGCGG
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCCG
GCTCTCAGCTACCCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAAGTAT
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTATCACAATGAGACCAACACAGAC
ACGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAATTACAAAGATAACCAACAACCAGAC
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCCGAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGCTGTGGAGACCA
GCTGTGTCTGTGGGTTCACTGCACCAAAATGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACA
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGC
ACACCCCTGCCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGCCCTCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGTGGGGGAGCCTGCGGCTG
CCGCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA
TAGAAATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCCTA
CATCTTCTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTGTGCAATTTGTTCACT
CCCCCAGGCTGTCTCCAGGCTTCACAGTCTGGTGTGCTTGGGAGAGTCAGGCAGGTTAACTGCA
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTGATAATTGTTTGGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTC
TGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAATG
CAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC
AGATGAAATGTTCTGTTCACCTGCATTACATGTGTTTATTCATCCAGCAGTGTTGCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT
CTCCACTACCCACACCAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACCTAATCTCACATCCCTCTAAAAGTAAA
CTACTGTTAGGAACAGCAGTGTTCTCACAGTGTGGGGCAGCCGTCTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCA
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG
TTTTCAGGTGTCATGGACTGTTGCCACCATGTATTATCCAGAGTTCTTAAAGTTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTGAGTTTAAATTATGTATAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL
 RSAVEEMEAEAAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMFSE
 TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMMLCTRDECCGDQLCVWGHC
 TKMATRGSNGTICDNQRDCQPGLCFAFQGRLLFPVCTPLPVEGELCHDPASRLDLITWELEPDG
 ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE
 RSLTEEMALGEPAAAAAALLGGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
 327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC
 GGCCACCTTGTGAACCTCGTGGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG
 GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCCTT
 AACTGGGTACTGGCCCTGGGCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT
 CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
 AACTGGGTACTGGCATTGGGAGCCCTCATCTGACCCTTGTGCAGATAGCCCGGTCATCTTG
 GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT
 CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA
 TCGCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC
 ATTTGTCAGGGTGGTCTGCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
 GGTCCGAGGCGTGGGGGTCCTGTCCTTCTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG
 ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCCTAT
 GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCT
 GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
 AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
 CCCTGATCCAGGACTGCACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT
 CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACT
 TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
 AAACCTCCGTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTATCCCA
 GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA
 GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAA
 AAGATTTTATTAAAGATATTTTGTTAACTC

FIGURE 10

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEFWTL
 NWVLALGQCIVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
 EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGNFCVSAKNAFMLLMRN
 IVRVVVLDKVTDLLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
 VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

FIGURE 11

GCGCCGCGCCCGGCGCGGGCGCCGAAGCCGGGAGCCACCGCCATGGGGGCCCTGCCTGGGAGCCTGC
 TCCCTGCTCAGCTGCGCGTCTGCGCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC
 CAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCTCTTCTTCTGCGGGTGTGGTGTCCA
 TCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGCC
 GGGATCCCCACCGTCTGACGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG
 CATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTTTACCCTGCTCATGCTCTGCGTGAGCAGCA
 GCCGGGACCCCGGGCTGCCATCCAGAATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTC
 ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCTTACCAACATCTGGTTCTACTTCGGCGCTCGTGGG
 CTCCTTCTCTTCATCCTCATCAGCTGGTGTGCTCATCGACTTTGCCCACTCCTGGAACACGCGGT
 GGCTGGGCAAGGCCGAGGAGTGGCATTCCCGTGCTGGTACGAGGCCTCTTCTTCTTCACTCTCCTC
 TTCTACTTGCTGTGATCGCGGCGGTGGCGCTGATGTTATGTACTACACTGAGCCAGCGGTGCCA
 CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTGCTG
 CCAAGGTCCAGGACGCCAGCCCAACTCGGTCTGCTGCAGGCCTCGGTATCACCTCTACACCATG
 TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCATTTGCCAACCAGCT
 GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG
 TGGGCCTCATCATCTTCTCTCTGTGCACCCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG
 AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTT
 GGCAGCCTGTGAGGGCGGGCCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC
 ACTTCTGCCTGGTGTGGCCTCACTGCACGTATGATGACGCTACCAACTGGTACAAGCCCGGTGAG
 ACCCGGAAGATGATCAGCACGTGGACCGCGGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT
 CCTCTACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCTCA
 CAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC
 CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCCTGAGCCGGG
 CTTCTAGTCGTAGTGCCCTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC
 ACCCACACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCCTGTTGCCCATACTCAGCATCTCGGATGAA
 AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCCACCACAG
 TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCAGTCCCCCAGGGGACCCTGCCCCCTTCTCTG
 GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCCTGTAAAAAAA

FIGURE 12

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRIFTFFLFLGVLVSIIMLSPGVESQL
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFTLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQRWLKAE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAACEGRAFDNEQDGVITYSY
SFFHFCVLASLHVMMLTNWYKPGETRKMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 13

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACACCTGCCAGAAGACATGGAGAACG
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTTCTTCTGGCAGTTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTCATTATC
CTTGCTGAGATTGAGACGTGGTTTCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTGAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG
GTCAGTTTTATTCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTAAATGTGAAAAACCTCACAGAAAGTC
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAATAAGGTGAAGAAAGTCTTGTGCTGTATTCCTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTTCATTTCAC
AGAATGGAATTTTTTGTGTTTCATGTCTCAGATTTATTTTGTATTTCTTTTTTAACACTCTACATT
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTTAAAAGTGTAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTCTGTTTTGCATTATGTGTATGGCCTGAAGTGTGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTT
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTGAATGC
ACAAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTGAGCCAATTTCAATTAAATGAA
CTAAATTAAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQIMARIESYEGREKKGISDVRRTFCLFVTFDLLF
VTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 16

MCSRVPLLLLLLLLLALGPGVQGCPSCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVFENGIT
MLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY
LGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLDLSSHNSLLALEPGILDTANVE
ALRLAGLGLQQLDEGLFSRLRNLHDLVDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL
AGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCLSWFGPWWRESHVTLASPEE
TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP
SPPSTAPPTVGPVPQDCPPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQGTSPSTP
VTPRPPRSLTLGIEFVSPTSLSRVGLQRYLQSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY
TVTQLRPNATYSVCVMPGPGRVPEGEEACGEHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV
LLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSE
CEVPLMGFPGLQSPHAKPYI

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
594-600, 640-646

FIGURE 17

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCCTCGG
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA
AAGGACCATACTACTGTCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGA
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAG
AAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG
CTACAACTTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAG
CAATAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG
GCAGCGAGAGAGATGTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTTGG
CTTTCTGTATGCCTCTGGACTTGGTGTAAATCAAGTCAGGCAAAGGCTCTTGTATATTATACAT
TTGGAGCTCTTGGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTTTAGTGGAAGGCT
ATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTTTTCAGCTTTTCATGATC
CAGATTTGCTTGTATTAAGACCAAATATTAGTTGAACTTCCTTCAAATCTTGTAAATGGATAT
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTTCTTTAAATGATTAG
TTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTTCTCTGAGTTG
GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA
AAATTTTGTAATGGTGGCTATAGAAAAACAACATGAAATATTATACAATATTTTGCAACAATGC
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTTCTG
TTTTTTACTTTTCATGATTGGCTGTCTTCCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT
GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTGTCTAATTTGG
AAGATTAACCTCATTTTAAATAAATATGTCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 18

MRVRIGLITLLCAVLLSLASASSDEEGSQDESLSKTTILTSDESVDHTTAGRVVAGQIFLDSESEL
 ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHGEPCHPFLFLDK
 EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRMQEAEMMYQTGMKILNGSNKKSQKR
 EAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFELTEEGSPKGQTALGFLYASGLGVN
 SSQAKALVYYTFGALGGNLIAMVLSRL

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 195-199, 217-221, 272-276

Tyrosine kinase phosphorylation site.

amino acids 220-228

N-myristoylation sites.

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

Glycosaminoglycan attachment site.

amino acids 267-271

Microbodies C-terminal targeting signal.

amino acids 299-303

Type II fibronectin collagen-binding domain protein.

amino acids 127-169

Fructose-bisphosphate aldolase class-II protein.

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAGCCCATTCTGCAGTGGAAATTCATGAACTAGCAAGAGGACACCATCTTCTT
 GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG
 CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAGACATCACTG
 ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACCTTTTGAT
 AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
 AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
 CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGTT
 CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
 CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
 TTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
 TATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
 ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC
 TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA
 AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
 CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
 TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
 GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
 AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT
 CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCAGGGT
 CCCTGCTCAAGTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCT
 GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAATTGAAAGACTTGCCCATTCAAAATGA
 TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACCTGTGAATGTTAAGT
 ATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAA

FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG
 CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTCTTCTTGGGGAAGTAAAA
 GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA
 CATTGAGAAATATATTCCATGCTATCAGCTTTTGTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
 AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATCCGT
 CGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACCTTGCAGGAGCATT
 TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
 ATCGACTGGAACATTCCCTTATATAAACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGGTT
 GCCAATCTGGGCATGCTGAACAACTGGGTTATAAACTGTATCAGGTTCCCTGTATGTCCACTGG
 TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG
 TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAGAGTATATGCAAAAAAGTG
 GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAACGAGAAATTGA
 GAAAGGAGAGGAGCACAGATTGAGGAGCAAGAGAGAAGAATCCAAAAAGACCTCAGGAGA
 ACATTTTTCTTTGTGAGGCACTTACGACCTTTTTTCCAAATTCTGAATTTCTTATTGATGTT
 ATGTCTTTAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACAACCATCTCGATGTAGT
 AGACATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC
 AAATCATTAAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA
 GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT
 GAGCAGCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
 CTACATTTTGATCCTTTTAACTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC
 ATTTCTATTGTTTTTACTATGTTGAGCTACTTGACGTAAGTTCATTTGTTTTTACTATGTTTACC
 TGTTTGACGTAATACACAGATAACTCTTAGTGCACTTACTTCACAAAGTACTTTTTCAAACATCA
 GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG
 ACACATTCTTTAGAATTGGAAGGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
 TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
 GAGACCATGTCTATTAAAAAATAAAATGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAA
 GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA
 CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
 AAAATTTAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLGGEVKGGEAKNSITDSQMDDVEVVYTTIDIQKYI
 PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL
 VLLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV
 QTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
 QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCYNHHLDDVVDNLTL
 MVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDQDKRSKANTGSSNQDKASKMSSPET
 DEEIEKMKGFGEYSRSPTF

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 75-79, 322-326

N-myristoylation site.

amino acids 184-154

Growth factor and cytokines receptors family.

amino acids 134-150

FIGURE 23

GGCACAGCCGCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCCAA
 GCAGCGCGCAGCGAACGCCCCGCCGCCACACCCCTCTGCGGTCCCCGCGGCGCCTGCCACCCCTTCCCTCCTTCCCC
 GCGTCCCCGCGCTCGCCGCCAGTCAGCTTGCCGGGTTCGCTGCCCGCGGAAACCCGAGGTACCAGCCCGCGCCTCT
 GCTTCCCTGGGCCGCGCGCCCTCCACGCCCTCCTTCTCCCTGGCCCGCGCCTGGCACCGGGACCGTTGCCTGA
 CGCGAGGCCAGCTCTACTTTTCGCCCGCGGTCTCCTCCGCTGCTCGCCTCTTCCACCAACTCCAACCTCCTTCTCCC
 TCCAGTCCACTCGCTAGTCCCCGACTCGGCCAGCCCTCGGCCCGCTGCCGTAGCGCGCTTCCCGTCCGGTCCCAA
 GGTGGGAACGCGTCCGCCCGGCCCGCACCATGGCACGGTTGGGCTTGCCCGCGCTTCTCTGCACCCCTGGCAGTGCTC
 AGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGACGCTTTTACGTGTCCAAAGGCTTC
 AACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCT
 CAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGAATCATTG
 CAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATTCTTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTG
 AATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAAATTTCTGAGCTATTTAAAGATCTCTTGTAGAGTTG
 AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATG
 TTCCGCTGCTGAACCTCCAGTACCCTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG
 CCCTTCGGAGATGTCCCTCGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTCTGCTCAAGGC
 TTAGCGGTTGCGGGAGATGTCTGTAGCAAGGTCTCCGTGGTAAACCCACAGCCCACTGTACCCATGCCCTGTTGAAG
 ATGATCTACTGCTCCCACTGCCGGGGTCTCGTGACTGTGAAGCCATGTTACAACACTGCTCAAACATCATGAGAGGC
 TGTTTGGCCAAACAGGGGATCTCGATTTTGAATGGAACAATTTCATAGATGCTATGCTGATGTTGGCAGAGAGGCTA
 GAGGGTCCCTTTCAACATTGAATCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT
 AATAGTGTTCAGTGTCTCAGAAGGTTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT
 TCCATCTCTGAAAGTGCCTTCAGTGCTCGCTTCAGACCACATCACCCGAGGAACGCCCAACCACAGCAGCTGGCACT
 AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTGGTCTCCCTTCCGAGCAAC
 GTTGTCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
 CTGTTTGCACTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAACCAGAC
 ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
 GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
 TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGTGGTGTCCGCTCCTGGGGCA
 CAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTTCTGGTTATGCAGAGAGAGTGGAGATTAATTCTCAAACCTGTGAG
 AAAAAGTGTTCATCAAAAAGTTAAAAGGCACCACTTATCACTTTTCTACCATCCTAGTGACTTTTGCTTTTAAATGAA
 TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGCTGACTTTGTTTTCTCATTCAGTTTGGG
 AGGAAAAGGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
 CTATAGTTAGTTGTGATTGTTGATTTTATCACTCTATTATTGTTGTATGTTTTTCTCATTTCGTTTGTGGGTT
 TTTTTTCCAACTGTGATCTCGCCTTGTTCCTTACAAGCAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATT
 TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
 CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH
 LYMQNSSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTE
 QLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL
 VTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
 MQDNSVQVSQKVFQGCQPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK
 EKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGSRYLFAVTGNGLANQGNPEVQVDT
 KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
 KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:**Signal peptide:**

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
 CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT
 TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
 TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
 CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG
 AGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT
 TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
 GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
 AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
 TTCTTCTCCACCTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
 TGTTTTTCAAGATCATTTTGTGTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
 GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAACTGTAGCTTCCT
 AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTT
 AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCTACCTGA
TGGCCGTGCTGACTCCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTG
CTCTGTGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTC
GAGCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA
GCAGAATGAGAGAAGACATTCTATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTC
CCAATGTTGTCCCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG,
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGL
 TGASGKVALLELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
 RQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPTW
 KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFSSKALICSFPSL
 QLEQATHQPIYLPLRGT

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

FIGURE 29

CAATGTTTGCCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAA
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTATTAAAGAAATT
GTTCCCTTCCCCGTGTTCATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
AGTTAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

· MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLLCLLPHRPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 31

GTTGAATTCCCTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT
 CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
 ATTTGCATCTGTTTTGATAAATGATGTTGACACCTCCACCGAATTCTAAGTGGAAATCATGTCGG
 GAAGAGATACAATCCTTGCCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC
 TTCAGATTTCATCACCACCTTCTGGTTCACATTTTCATTTTCATTGGTTATTTTGGGATTGTTGTT
 TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
 CAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGTCTATCGTATCCACAGGCATCACGGCAGTG
 CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC
 AAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA
 TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAACTGCAGGAGCTGCCCAGGTT
 ATGGAAGGCGGCCAAGTGGAAATATAAGCCCCCTTCGGGCATTGGGTACATGTGGTTCGTACCATTT
 AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG
 TGGTTACTTGTATTTCACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTC
 TCCATTCTCTTCTTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG
 GATTCCGAGAATCATTTGTCATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCAATTGT
 CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
 AACCAGAATGCATATACTAACAAGTCTATTAATGGGACAGATTCTGTACATCAGCAAAAGATGC
 ATTCAAAATCTTGTCGAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA
 TTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC
 AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC
 CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCCTGTGTTTGTCTGTTGATC
 TGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
 AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA
 GGGAAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
 TCCTTCTAAGAGCCATTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT
 TTAAGACCTAATAAACCTATTCTTCCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYDNDLSIE
 LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTF
 ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA
 GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQLKEQQHG
 ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
 FIIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA
 VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

Important features:

Signal peptide:

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
 CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSLPRWR
 ESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPIPGTTAQPVTLMQLLAVTVAVA
 TPTTLPRPSPSAASTTSSIPRQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP
 VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
 GPAGPLMGVVQYGDNPATFNKTHNTSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
 RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENKQYVVEPNFANKAVCRTNG
 FYSLHVQSWFGLHKTLOPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
 LTKEFEISDSTDTRIGAVQYTYEQRLIEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQL
 FKKS KPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFF
 VDEFDNLHQYVPRIIQNICTEFNSQPRN

Important features:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
 431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

Amidation site.

amino acids 304-308

FIGURE 35

CCGAGCACAGGAGATTGCCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC
 CAAACCATGTCTTTTTTCTGTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT
 ACAGAAAACAACAAAAAATTAAGCTTTAATTTTCATCTGGAATTCACAGTTTCTTAGCTCCCTGGACCC
 GGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCGAGTGTA
 AAGAACCCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCTTCCGAGTA
 GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC
 CTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTTA
 CAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAACCTGCTCTCATCAAAATCCATTTCTGGTCATTC
 TGGTGACCTCCACCCCTTCAGATGTGAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT
 TGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGC
 ATGTGCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA
 ACCTGACCTTGAAAACATTATGGCATTGAGGTGGGTAAGTGAATTTTGGCCCAATGCCAAGTACGTAATG
 AAGACAGACACTGATGTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA
 GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATATTT
 CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAATGTCCAGAGAT
 TTGGTGCCAAGGATCTATGAAATGATGGGTACGTAACCCATCAAGTTTGAAGATGTTTATGTCTGGGAT
 CTGTTTGAATTTATTAAAAGTGAACATTCATATTCAGAAGACACAAATCTTTCTTTCTATATAGAATCC
 ATTTGGATGTCTGTCAACTGAGACGTCTGATTGCAGCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT
 TGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAAGTTCACATTCTACAAAAGCCTAGAAGGACAG
 GATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTCTGGCTT
 ACACTGAACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG
 CCGTTCAAAGATGATATGTGGAGGAATTAATATATAAGGAATTGGAGCTTTTTGCTAAAGAAATTAATAGG
 ACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGGTGTACTGAGTTATAAGCTCA
 CTAGGCTGTAAAAACAAAACAATGTAGAGTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTGTGTA
 TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACCTTCTTCACTGAAGTTATA
 CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT
 ATTTATTTAAATTAACCTTCACTTTGTGTTTTTAAATGTTTTGACGATTCAATACAAGATAAAAAGGATAG
 TGAATCATTCTTTACATGCAACATTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA
 TTAATGTAAAGTCATAGGTCAATTATGCATATCAGTAATCTCTTGGACTTTGTTAAATATTTTACTGTGGT
 AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKEDKMLA
LSLEDEHLLYGDIIRQDFLDYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYL
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSKEIITFWQVMLR
NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRCGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII
KRVCGNERPAPIQSIGSSLHVLHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNSNVLSGNE
KRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPHQLYSAAFSKQKLQSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
KTQGLRWPQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFAQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLFPKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTACGGGCCCGTGATTTATTAACGTGGCTTAATC
 TGAAGGTTCTCAGTCAAATTCCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
 TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGCTTCTGTTGC
 TGGTCTTGCCTTGGCTCAGTCTGTAACTACATTGACAATGTGGCAACCTGCACCTCCTGTATTGAGAACTCTGTA
 AAGGTGCCTCCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC
 TCACAGCCACGGCTCCCTCCCCAGAGGTTCTGCGAGCTGCCACCATCTCCTTAATGACAGACGAGCCTGGCCTAGACA
 ACCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCACTGGACTCTGGCCGGAGCAACCGAACTA
 GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA
 GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGAAAAATTCTGAAAACACCACTGCCCTGAAG
 TCTTTCCAAGGTTGTACCACCTGATTCCAGATGTTGAAATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAAA
 GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTTACCAACACATTTATCGTGATGGGG
 TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC
 ACAACTACGCTGTGCGTCTCTCGCGCAGCCCTGCCAGGTGTGTGGCTGACTGTGATGCGTGAACAGAACTCCGCA
 GCAGGAACAATGGACAGGCCCGGATGCCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC
 CCAGAGGACGAGCTTGAATAAACTGGTGCAGCAAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGTGGATGGCG
 GTGTGGCATATCGACATGCTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA
 GCCCAGAAAGTGGCGCTCATCTGATTGAGGCCAGTGAAAGACGTGTTACCTCGTCTGTCCCGCCAGGTTTCGGCAGC
 GGAGCCCTGACATCTTTAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCAGGGCCAGGGGAGAGGAGCAACA
 CTCCCAAGCCCTCCATCCTACAATTACTTGTCTATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCG
 GCATGACCGTCGCAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCTCAGTGTTGAGCCCGGAGGAG
 TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTGAGCC
 GGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC
 CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT
 GGGTCATGTGGCTGGAATTACCACGGTGCTTGTATACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC
 TGGGCTTCTGCATTGTAGGAGTTATGAAGAATACAATGGAACAAACCTTTTTCATCAAATCCATTGTTGAAGGAA
 CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGTCTCAATGGTGAAGTACATCAGGAATGA
 TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTCTTGGCCTGGCACTT
 TTTTATAGAAATCAATGATGGGTGAGAGGAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTTATC
 TTGTGAGTTTTTATATTTAAAGAAAGAAATACATTTGTAATAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
 ACACCTCAGAAAATATGATTCAAAAAAATTAATACTACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTAC
 AACATTGTTTATATTTTTCTATTCAATAAAAAAGCCCTAAAACACTAAATGATTGATTTGTATACCCCACTGAATT
 CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTTACAGCT
 AAAATATTTTTTAAATGCATTGCTGAGAAACGTGCTTTCATCAAACAAGAATAAATATTTTTCAGAAGTTAAA

FIGURE 40

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS
 PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINR
 ALSVLRRTKSGSAVANHADQGRESENTTAPFVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV
 GGSETPLVHIIIIQHIIYRDGVIARDGRLPGDIIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM
 REQKFRSRNNGQAPDAYRPRDDSFHVLNKSSPEEQLGIKLVKRVDEPGVFIFNVLDGGVAYRHH
 QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQRSPDIFQEAGWNSNGSWSPG
 PGERSENTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR
 IKTGDILLNVVGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP
 SDWSPSWMMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG
 RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
 467-473, 603-609

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
 CTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGCCTCAACCTGACT
 TTCCACCTTTCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC
 CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCTTAAAGCAAAGGAGTTCATGGCTAATTTCC
 ATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAAGTT
 GACAACCTGTCCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACAGATCTCAC
 TTTGGAAGAGGTACAGGCAGAAAAATCCCAAAGTGTCCAGAGGCCGCTATCGCCCTCAGGAATGTAAAG
 CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
 CATCTGCATCCCTTCCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
 TAAAAAGTTTAAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
 ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
 CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGG
 GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACCTACTGGGGAT
 GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
 CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
 GATGAAGCTCTTACACCAAGTGTACAGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT
 TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTCTGGTTTGGTGCATGACCCC
 TGGATCTTTTGGTGATGTTTGAAGAAGTATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAA
 ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTGTATTTTCT
 TAGCAGAGCTCCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGAT
 CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
 AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGAT
 AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
 AGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGTCAGGT
 GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA
 GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
 CTTACAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT
 TTTTAAAGAGTTTTTGTAATATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
 ATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

FIGURE 42

MGFNLTfHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTILGKGKTLTN
 EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH
 RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV
 DLVPENDFNLYKCEEHPKHLVVGGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWWGED
 DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV
 SVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 43

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG
 CCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCACAAACAG
 ACGGGACAACCTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT
 GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC
 ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCCGTCCCCCTCCC
 TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTTGTTT
 TCCAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 44

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCCHRSKCGMCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

FIGURE 45

GTGGCTTCATTTCACTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG
GACCTTCAACACAACCCCTCTTGTCCACATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTCAGCAGAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG
GTCCTCCTGTGTCTCCTGTTGGTGGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCCTCCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
 EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
 PKVTMGLQSNKNGTCVTNLTCMEHGEEVDIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
 VARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLSLFLVLGLFLWFLKREERQEEYIE
 EKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLTMDPT
 PRLFAYENVI

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
 291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
 ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
 TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT
 ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
 CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTCCTGAGTGTGATCACAGTCATTGGTGCTC
 TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCTCTCATGTGTAATTCTCCAAGC
 AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA
 CTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG
 ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
 CTTATCCACTTCTCAGTATTTTAGGTCTATTGCTTGGTGAATTCTGGAGGTCTGTTTGGGCT
 CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
 TGTAGTTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

FIGURE 48

MTCCEGWTSCNGFSLILVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
 TTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNANCEFSL
 KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL
 LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:**Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA
 AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG
 ATCCGTGGGCTGCAGACCCCGCCCCAGTGCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA
CATGGAGAGAGTGACCCGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC
 CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
 TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
 CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCCTCATCACTCCAGGCTCTGCCA
 CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
 TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCCCT
 TTCTGATCAGGAGGCTTCTTTATGAATTAACTCGCCCCACCACCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCKYKS
SQKQHSPVPEKAIP LITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG
 AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG
 AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG
 GGGCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG
 CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA
 GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGCAGCTGGCTCTAAAGTCAGTGAG
 GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC
 AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA
 TTGGCAGACAGGCAGAAGATGTCATTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG
 GTGCCTGGCCACAGTGGTGTCTGGGAAACTTCTGGAGGCCATGGCCTTTGGCTCTCAAGGTGG
 CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG
 GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA
 GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAAGTGAG
 AGCCAGCAACCAGAATGAAGGGTGACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA
 ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC
 AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG
 TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT
 CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA
 CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGGGAGCGGGGAATCTGGGATTCAAGG
 CTTAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG
 GAGGCTCTGGAGACAATTATCGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT
 GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTAACTTTGACACTTTCTGGAA
 GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC
 GCATCCCGTGACCCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACACTCCCTCCTTAA
 AACACCACCCTCTCATCTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA
 AA
 AA

FIGURE 52

MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS
EALCQGTREAVGTGVRQVPFGGAADALGNRVGEAAHALGNTGHEIGROAEDVIRHGADAVRGSWQGV
GHSGAWETSGGHGIFGSQGGGLGGQCGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNF
GTNTQGAVAPGYGVSVRASNQNEGCTNPPPSGGGSSNSGGGSGSQSGSSGSGSNGDNNGSSSSGGS
SSGSSSSSSSGSSGGSSGGSSGNSGGSRGDSGSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNE
ARGSGESGIQGRGQGVSSNMREISKEGNRLGGSGDNYRGQSSWGSGGGDAVGGVNTVNSETPGM
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCCGCCGGCTCCAGTGTTC
CACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC
TTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT
GAAGTCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGCTGGACATGTTTGGACACATCAGCCTCATGACCTTGGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGGCCAGTGAATATATTGCCACCAT
CTTGGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC
GCTGTCATCCGGGAGCGGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCAG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGGATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTCCGCA
GGGCCAGGAACTGCATCGGGCAGGCGTTCCGCATGGCGGAGATGAAAGTGGTCTGGCGTTGAT
GCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAATTGATCATGC
GCGCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGACAGTGACTTTCTGAC
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWGHLG
 LITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
 WLGEGLSSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
 SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
 RLVHDFDPAVIRERRRTLPTQGIDDFKDKAKSKTLDLFDVLLLSKDEDGKALSDEDIRAEADTF
 MFGGHDTTASGLSWVLYNLAHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
 LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP
 LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN
 VGLQ

Important features:

Transmembrane domains:

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA
 GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT
 TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG
 TACAGCCTTTCCTTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTTTTGCCGTGTGTCTTGC
ATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT
 GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTTGCTT
 GTGATTGGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA
 GCACAGGATGAGAAGTGGGTCTGTATCTTGTGGAGTGAATCTTCCTCATGTACCTGTTTCCTC
 TCTGGATGTTGTCCCACTGAATTCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAAAAA
 AA

FIGURE 57

[illegible]

FIGURE 58

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLG
 QLDFFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILKSMDKNG
 TMTIDWNEWDRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG
 AGAVSRTCTAPLDRLKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIAK
 FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQAQSSIYPMEVLKTRMALRKTGOYSGMLDCARR
 ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTC
 GQLASYPLALVRTRMQAASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV
 VYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
 TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
 CACTCATCATTGGCTTTGGTATTTGAGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCT
 GGGAAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTCTGATAT
 CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
 AGCTGTGCGAGCAGGATGAAATGTTTCAAGGCGGACAGCAGTGTGTTGTGATCAAGTGATAGTT
 GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
 CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
 AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC
 CAGCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATAC
 CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA
 TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
 ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGTAAACTCAAAGGCTTCTCTGTGTGT
 CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT
 GTGCCCTTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAATATTTTAC
 CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
 AGCAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
 CTATCTTCAAAGACATATTAGAAGTTGGGAAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGA
 GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
 CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTGTATATGTGC
 TGTAAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCAC
 AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
 GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCCTTGGCTTC
 TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
 CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6o

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
 DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLRLKNVQLTDAGTYKC
 YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS
 NTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESIKRRLSHLQLLNSKASL
 CVSSFFAISWALLPLSPYLMLK

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
 220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG
 CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
 GGGCTACCCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG
 TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCCTCTGGAATCCAGGAGGACCATATG
 GCGGTGCAGCTCCCGGGGGCCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCAGCAGCCT
 GGGCTTTATGGACAGGGTGGCGCCCCTCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
 GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
 ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
 GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAGAACCTCTT
 CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
 AAATGGGCTACAACTGAGCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT
 GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
 GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
 CCATGACAGCTTCTCGGATGCTATGACCCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
 TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTCTTTTCTGTCCCTCTAGAAGAAC
 ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTTGCATCATAGCCACCA
 AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCCCTGATGGAGGAGAGGATAGAAGTTGA
 ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGG
 AGTTAGTGTCCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTCATCGGCCTGTTACC
 GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCATTTTCTCCAAAGTGGAAT
 CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGATTCTGCCACACCCATAAAT
 CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
 CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT
 TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTTGCATTTTTTTTC
 ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
 HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDS DH
 SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
 DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK
 DTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
 66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

CAGGATGCAGGGCCGCTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC
TCCCAGGCCTCTTTGCCCGGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC
AACTTGCCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGC
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCTCTGAAGCTCAGCGTGCCTCCATCAGATG
GCTTCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG
GATTCCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA
AGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGCTGCGGCCCTCGCTCCGGGCAGTGGCCCTT
TGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC
TCGGAGTCCAGACGACTGCCCCGTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACG
CCCTCCCTGGTCTCTCATCCACAGGGTTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTG
TGTCCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG
GCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCCTGGAGTCTCCGC
CCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG
GGGCTAGAGCACGATAGAGGGAACCCCAACATTGGGAGTTAGAGTCTGCTCCCGCCCCCTGCTG
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 64

MQGRVAGSCAPLGILLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSQVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRNSNLGAGGKILSQRP
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIWGINNQPPGTSGWNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFVLRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 66

MGSGLPVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCAGTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT
GCCGCCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
AGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLLALGLPFLRLRWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVFS
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTTCAGAGGTTTTGTTTTCTCTTAGTTCTGTGCCTGCTGCACCAG
TCAAATACTTCTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA
GATGAAAAAATAATGAACAAATAGAGGATATGGTACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA
TTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAACATGAA
AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCATACACCAAGCAGTTTACA
GAATGTGGAGAGAAAGGCGAATACATTCACTTCACCCCTGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA
CCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGATGAGTACAATGAAGATCAGCCTTTC
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT
CAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACCTGTATGGAAAAGATTGTCAATTCTTT
CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAA
AAAAACCATTAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGAATTTTAGAAGTACATGGGAGGTGATTAGCAAT
TCTGAGGATTTTAAAAACACCATAACCCATGGTGACACCACCTCCTCCACCTGTCTCTCATTGCTGAAGATCAGTCAA
AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTGAAGGACCGCCTAAATCGAATGAATCAAGCAGCA
AAACATTTCTGCTGCAGACTGTTGAAAAATGGATCCTGGGTGGGGATGGTTCATTTGATAGTACTGCCACTATTGTA
AATAAGCTAATCCAATAAAAAAGCAGTGATGAAAGAAACACACTCATTGGCAGGATTACCTACATATCCTCTGGGAGGA
ACTTCCATCTGCTCTGGAAATAAATATGCATTTCAGGTGATTGGAGAGCTACATTTCCAACTCGATGGATCCGAAGTA
CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGATTGATGAAGTGAACAAAGTGGGGCATTGTTTCAT
TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT
TCAGATGAAGCTCAGAACATGGCCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAAAG
TCCCTTCAGCTCGAAAGTAAGGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCATAATTGATAGTACA
GTGGGAAAGGACACGTTCTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCCACTGGAACA
ATAATGGAAAATTCACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAACTGCAAGGTGGGCACT
TGGGCATACAATCTTCAAGCCAAAGCGAACCAGAAACATTAACIATTACAGTAACCTTCTCGAGCAGCAAAATCTTCT
GTGCCCTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAAACAGTTTCCCAAGCCCAATGATTGTTTACGCAGAA
ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT
TTGGAACCTTTGGATAATGGTGCAGGCGCTGATTCTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT
ACAGAAAATGGCAGATATAGCTTAAAGTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAAATACGGCCTCCA
CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAACCCGCAAGACCTGAAATTTGAT
GAGGATACTCAGACCACCTTGGAGGATTTCAAGCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAGTCCCAAGC
CTTCCCTTGCTGACCAATACCCACCAAGTCAATCACAGACCTTGATGCCACAGTTTCATGAGGATAAGATTATCTT
ACATGGACAGCACCAGGAGATAATTTGATGTTGAAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT
GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACAAAGGAGGCCAACTCCAAGGAA
AGCTTTGCATTTAAACCAGAAAAATATCTCAGAAGAAAATGCAACCACATATTTATGGCATTAAAAATATAGATAAA
AGCAATTTGACATCAAAAGTATCCAACATTGCACAAGTAACCTTTGTTTATCCCTCAAGCAAATCCTGATGACATTGAT
CCTACACCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTGGTATTTG
TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACCACATTGGAACCTTAACGAAGAAAAAATCTTC
AAGTAGACCTAGAAGAGAGTTTTAAAAACAAAACAATGTAAGTAAAGGATATTCTGAATCTTAAATTCATCCCAT
GTGTGATCATAACTCATAAAAATAATTTAAGATGTCCGAAAGGATACCTTTGATTAAATAAAACACTCATGGATA
TGTA AAAAAGTGTCAAGATTAATAATTTAATAGTTTCATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAACAAAG
ATCCTTTTTCATACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTCTGAAATGATATTTCAAATTCATCAA
GAAATTAATAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGGCAAAATAACAACATTTGGA AAAAAAAAAA
AA

FIGURE 70

MGLFRGFVFLVLCLLHQSNSTFIKLNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTYLFE
 ATEKRFFFKNVSLIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
 IHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISGRN
 RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVEFCNEKTHNQEAP
 SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLVLDKSGSMGGKDRNLNR
 MNQAAKHFLQLTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK
 YAFQVIGELHSQLDGSEVLLLTGDNNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
 SHFYVSDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
 ITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR
 AANSSVPPITVNAKMNDVNSFFSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
 GADSFKNMGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRPPLNRAAYIPGWVNGEIEANPP
 RPEIDEDTQTLEDFSRASGGAFVVSQVPSLPLPDQYPPSQITDLATVHEDKIILTWTAPGDN
 FVDGKVQRYIIRISASILDLRDSFDDALQVNTDLSPKANSKESFAFKPENISEENATHIFIAI
 KSIDKSNLTSKVSANIAQVTLFIPQANPDDIDPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI
 VNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 71

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGGGCAGGGGTGA
CAACAGGTGTCTCTTTTGTATCTCGTGTGGCTGCCTTCCTATTTCAAGGAAAGACGCCAAGGTAATTTTGACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTGTGGTTGGAGGAGAGAACCCTTTGTGGGGCTGCCTTCTCTTAGCA
GTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAGAAGAAAGGAAAGGTPCCCTCTTGTCTGTGGCTGCACATCAGGAA
GGCTGTGATGGGAATGAAGGTGAAAACCTGGAGATTTCACCTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAA
AGTAGAGAAGCTGCTCTGTGTGGTGAACCTCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAAACGCATGCTTCCTGTGGTCTAGCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCTTTGAGGGATGCC
ACCGGTTCTGGACGCATGGCTGATTCCCTGAATGATGATGGTTCCCGGGGGGCTGCTTGCCTGGATTTCCTGGGTGGTG
GTTTTGCTGGTGCTCCTCTGCTGTCTATCTCTGTCTGTACATGTTGGCCTGCACCCCAAAGGTGACGAGGAGCAG
CTGGCACTGCCCAGGGCCCAACAGCCCCACGGGGAAGGAGGGGTACCAGGCCCTCCTTCAGGAGTGGGAGGAGCAGCAC
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGG
AATGGGCAGTACCAAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC
CTGGCCCTCCTGCCTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGATATGCAGCAGTG
CCTTTCCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCGAGGAGAAGCCTGTG
AGGAAGGACAAGCGGGATGAGTTGGTGGAGCCATTGAATCAGCCTTGGAGACCTTGAACAATCTGCAGAGAACAGC
CCCAATCACCCTCTTACACGGCCTCTGATTTCATAGAAGGATCTACCGAACAGAAAGGACAAAGGACATTTGTAT
GAGCTCACCTTCAAAGGGGACCAACACAGAAATTCAAACGGCTCATCTTATTTGACCATTTCAGCCCCATCATGAAA
GTGAAAAATGAAAGCTCAACATGGCCAAACAGCTTATCAATGTTATCGTGCCTTAGCAAAAAGGGTGGACAAGTTC
CGGCAGTTCATGCAGAATTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTACTTTGGG
AAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAACACCTTCCAAAGCTGCCAATTCAGGAATTTACCTTCATC
CAGCTGAATGGAGAAATTTCTCGGGGAAAGGGACTTGATGTTGGAGCCGCTTCTGGAGGGAAGCAACGTCCTTCTC
TTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAG
GTATTTTATCCAGTTCTTTTCAGTCACTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA
CAGCAGCTGGTCATAAAGAAGGAAATCGGATTTTGGAGAGACTTTGGATTGGGATGACGTGTCACTATCGGTGCAGAC
TTCATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCCGAAGTATCTC
CACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTG
GTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAAAACAGAAACAGAAACAGTACGAAAAAACA**TGA**ACTCCAGAG
GAAGGATTTGGGAGACACTTTTCTTCTCTTTTGCATTTACTGAAAGTGGCTGCAACAGAGAAAGACTTCCATAAA
GGACGACAAAAGAAATTGGACTGATGGGTCAAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTACACAGAG
AATCAAAATCTCCGCTTTCCTGCAAAAGTAACCCAGTTGCACCTCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG
AGATTATAAGCCTAATGGTGTGGAGGTTTGTATGGTGTTTACAATACACTGAGACCTGTTGTTTGTGTCTCATTTGA
AATATTTCATGATTTAAGAGCAGTTTGTGAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAATATCAGAAGGCAGGAGAGATAGGCTTATATGATAGT
AGTGAGTACATTAAGTAAATAAAATGGACAGAAAAAGAAAGAAACCATAAATATCGTGTCTATTTTCCCCAAGAT
TAACCAAAAATAATCTGCTTATCTTTTGGTGTCTCTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCCT
TTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTAC
ATTTTTATATTTTTTAAAGAGATACTTTGAGATGCATTATGAGAACTTTTCAGTTCAAAGCATCAAAATGATGCCATAT
CCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTTGTACT
AATACAGACGTACAGATACTTTCTCTGAAGATATTTTGAAGAGGAGCAACTGAACACTGGAGGAAAAAGAAATGAC
ACTTTCTGCTTTACAGAAAAGGAACTCATTGAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCATTTT
CTCTCAGAAGTAGGACCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACCATCTCTTTTC
AAAACAGGGTGTCTCTCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAAATATATATATATATATATATTGT
GAAAGATCAATCCATCTGCCAGAATCAGTGGGATGGAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAG
TAAGTGAATTTATTTTAAATTAAGCAGTTCTACTCAATCACCAAGATGCTTCTGAAAATGCAATTTTATACCAATTT
CAAATATTTTAAAAATAAATACAGTTAAACATAGAGTGGTTTCTTCTCATGTGAAAAATTTAGCCAGCACCAG
ATGCATGAGCTAATTTATCTTTGAGTCTTGTCTTGTCTGCTCACAGTAAACTCATTTGTTTAAAGCTTCAAGAAC
ATTCAAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTTGTACTGGTAGTTTATGAAATTTAATTAACACAGG
CCATGAATGGAAGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ
PHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQINSEAT
FAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKRLNRKS
VVETSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGCGGACGGGCAGTTCCCTGTGTC
TCTGGTGGTTTGCCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCTGACAGCTCC
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGTCTACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCTTTCGTCCC
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTGGCCATATCTATTACCGTGTTCCTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT
GATTTTGATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCCGTGCTGAAAAATCGTGATTA
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAATTTTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTCACCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAA
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCCCTGAAGAGCAGGA
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCCGAGGCAGCGTTGGCAG
TCTTGGGCCCCGAAACGTTACAGTACTCATACCCCCCTCAGCTCCAAGACTTAGACCCCTGGCG
CAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA
TCCCCAACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA
TGTGCAGATGGAAAACGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAG
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT
CTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

FIGURE 76

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY
 SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK
 DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDKRFFVPAEK
 IVINFITLNISSDKISHQDMSLLGKSSDVSSINDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
 DSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVVRTTDICAGPEEQELSLQEEVSTQGTLLSQA
 ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRCLPSLSSFDQDS
 EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
 CTGGGAAGATGGCCGCCCCGTGGACCTTCACCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
 CAAGCCACCCTCAGTCCCCTGCACTTCTCATCCTCGGCCCAAAGTCATCAAAGAAAAGCTGAC
 ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
 GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC
 ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
 GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCA
 TCGTGGAGTTCCACATGACGACTGAGGCCAAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC
 CCCACCCGCCCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTCTGTGA
 TAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGC
 CCAATCTAGTGAAAAACAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
 CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTGA
 TCCTGCCATCAAGGGTGACACCATTACAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA
 AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG
 TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
 ATTCATGGTCCTGTTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
 TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
 ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT
 TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
 TTTACACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTG
 ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
 CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTGATTGGTGAAGG
 CCTTGGGATTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC
 TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG
 GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACAATTG
 CCTGTGAAAAA

FIGURE 78

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDNATSILQQLPILLSAMREK
 PAGGIPVLGSLVNTVLKHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE
 FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
 VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYLGAKLKLLDSQGKVT
 KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVLPESAHLKSSIGLIN
 EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGLIEASSEAQFYT
 KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSVGPVSLVKALG
 FEAAESSLTkdalvltpaslwkpsSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGGCCTCCAACCTTGTTGGGTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGAGGGCTCCTGGGATTC
ATTCTGTGGCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACCTACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCCTACAGCCTGACAGGGTATGTGTCAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCTGCCCTAAGTCCCCAACCCCTCAACTGAAACCCCATTCCTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCACTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD
IYSTLLGLPADIQAAQAMMTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCTTCTGCTCTCCATCTCTCCCTCCTTTC
 CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTGCCCTCCTTTCCCT
 GCCCACCGCTGCTTCTGCCCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
 GTTGATCTGTGGCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCTTCCGACTCCGCTCCCGG
 ACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTCTCCTTGTGTGGGA
 CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT
 CCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT
 ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCCT
 GTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCAAGTGTGTGGAACCTCACAC
 TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACAAACGGGACCATGTACCAACACGGAG
 AGATCTTCAGTGCCCATGAGCTGTTCCCCCTCCCGCCTGCCCAACCAGTGTGTCTCTGCAGCTGC
 ACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCGAACCAGGCTGCCCAGCACCCCTCCC
 ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGGAGGACA
 GTGTGCAGTCGCTCCATGGGGTGAACATCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG
 AGAGGCCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
 CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCT
 GTGTGCATGGCGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
 CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
 CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGG
 ACAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGGTC
 CTCGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC
 CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG
 GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG
 GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCACGAAGTCACT
 GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG
 ACATAACAAAGACCTTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATATTAATAAA
 TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGPPTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTY
HGEVWHPAFRAFGLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKQVAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRFALEHEASDLVEIYLWKLKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPPRSLERLPSDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGGCCCTCCGCTCACGCAGAGCCTCTCC
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTCTCTAATCCATCCGTCACCTCTCCTGTCA
TCCGT'TCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAG
CACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGGCGTTCTTCAGGGG
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTA
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT
ACAGGTGTACGACTGGGCTCAGTTCCCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC
TCTGTACGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTGTGCC
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGTGTGGAGATCTCTCTGACCGTCCAAGAGAA
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG
GAGATACCTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
TTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATCCAGTGGAAAATCCAGGCGGAACTGGACTG
GAGAAGAAAGCACGGACAGGCAGAAATTGAGACACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAG
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATAGAAAAGCTCCCCAGGAGGTG
CCTCACTCTGAGAACAGATTACAAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAACATTA
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT
ACATTAAATCCCCGTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTA
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGTTTG
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTTATAATGAGCAAAATGGAATCCCATAGTCATCTGC
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCAGAGACAAGCAACAG
TGAGTCCTCTCACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGCCAAGGTGCCTTCCA
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCTGGCTGCCCTGAGCTGGGAGGGAAGAAGG
CTGACATTACATTTAGTTTGCTCTCACTCCATCTGGCTAAGTATCTTGAATACCACCTCTCAGGTGAAG
AACCGTCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG
ATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

FIGURE 84

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFPPTAKWKGPQGDLSTDSRTNRMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEVPHSEKRF
TRKSVVASQSFQAGKHYWEVDGGHNRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT
LNPRFISVFPPTPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPESTNSSESSQATTPFLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
 CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAAATGAACCAACTCAGCTTCCTGCTGTTTC
 TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
 TCTTCGCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCAATTGA
 TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
 GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
 GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
 CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
 ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCATGCAGCACTGG
 AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
 GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
 CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCTAT
 GGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
 CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
 GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
 GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
 TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAA
 CAACTTACCCAGTAGCTAGAATGTAAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
 AAAAAA

FIGURE 88

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
 YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAAT
 SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGLIYQKYPVKYG
 EGKCWTDNGPVIIPVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAANALCAGMRVTGCN
 TEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGAC
CGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTCGCCCTCTCGCTTCTTGACG
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGACAGCAACATACAGGCCTG
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCT
CTGTCACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGAGTCTCCATGTTCAAC
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT
ATTGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTGTCTTCTGCAGTGGCCCTTCCAGCTG
TCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTGTATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFV
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCCCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT
GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC
CACCCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCGCCGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG
CTCCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTAC
CATAGTGATACCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTC
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCGTGTGCTGAGCATGG
CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCTGTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAAGCCTCACCTGTCAGACCGGGGTCTCCCGGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGAGCATGTGCTGGATCTGTTC
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGAAGTCTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAGCTTGCCCCGGGGCA

FIGURE 92

MQLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEANGILGPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCCTTCGGGCCTGCGCTCGCC
 CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT
 CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTGGTTTCATGGCAAGAGTCATTATTGACAACA
 AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA
 ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
 AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTCTGGCTTGGGCTTTGGAATCATGA
 GTGGAGTATTTTCCTTTGTGAATACCCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT
 GGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTTCATGACGCTGGTCATTATCTTGCTGCATGT
 ATTCTGGGGCATTGTATTTTTTGGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
 TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
 TCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
 AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAAGTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
 TTTTCTGAAAATCCCTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 95

AATTTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG
 GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC
 TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTCCGGATCAGG
 GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAACA
 CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC
 CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTAC
 CAATTTTTGTACACAACCTTGAGAGCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC
 TTCACGAGCCTCATCATCCATTCCCTTGTTCCCGGGAGGCATCCTGCCACCAGTCAGGCAGGGGC
 TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAATCCTGCCACCCAGG
 GAACCCAGCAGGCCGCCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT
 GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
 GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC
 ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT
 TACCTGAAAATATTCTTGAAATTTAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA
 CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
 TAAACATATTTGGAAAACTGGAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQSNOVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPFI FVTQLGAQG TILSSEE
LPQIFTSLSIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTT PAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTGACCATG
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGCCAGCCTGC
 AGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGAAATTTCCCTTTATACCTGACCAAGTTGC
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGTGTGAGGGGACTCAGGCAAGGCAACTGAG
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCCCTGCTGGTGACCAGGGCCCTGGACCGAGAGGA
 GCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCATTTCTCTCAAGCCATCTAC
 AGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCCCCTTCCCTTCTCCTTGAGGCTTCAGACCG
 GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCCTGAGCCAGGCTCCAGCCAGC
 CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
 ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
 CCAGGCCCTCAGGCCACCAGGCCACTGCCACCGTGGAGTCTCCATCATAGAGACACCTGGGTGT
 CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCCCTATACCCGCACCACATGGCCCAAGGTA
 CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCCGGGACCCCTTGAAGTGAA
 TGCAGAGGGAAACCTTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC
 AGGTGCGGGCTCAGAATTTCCATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTG
 ATGGATGAGAATGACAACGTGCCCTATCTGCCCTCCCCGTGACCCACAGTCAGCTCAGCTGAGCT
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGACAGAGGATGACATGCCCCGGCTCCCCCA
 ATTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
 CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
 TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCACTTCCCAGATTGGGCCCT
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
 CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCC
 AGGCCCTGGAGCCACCGCCACGGTGAAGTGTGCTAGTGGAGAGAGTATGCCACCCCCCAAGTTGG
 ACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCCAGCCGGCTCTTTCTGTCTGACCATC
 CAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
 CTGCATTGAGAAATTTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
 ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCCAA
 TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGAGCCAGCAAGGACCCCGATCT
 GGCCAGTGGGCACGGTCCCTACAGCTTACCCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGT
 GAACACATAATCCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGAT
 CGTGTGTGCGTGCAACGTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCTCATCCTC
 , ATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCCT
 GAAGGCGACTGTCTTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATGTAG
 TCCCCCTGGGAGAGAGCCAGCACCCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCA
 TCTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAACTT
 TATGGACTGCCCATGGGAGTGCTCCAAATGTGAGGCTGTTTGCCCAATAATAAAGCCCCAGAGAA
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSVPQALPKAQPAELSVPEVNYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT
 EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI
 YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG
 STSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ
 VHWGGDVHYHLESHPPGPFVEVNAEGLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
 VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
 FQVDPTSGSVTLGVLPRLRAGONILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG
 PISLPEDVEPGTLVAMLTADADLEPAFRIMDFAIERGDTEGTGFLDWEPPDSGHVRLRLCKNLSY
 EAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT
 IQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTLPVPS
 QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTALHWWVEP
 REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTILVAIGIFLI
 LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
AVGLFAGLFFCVRNSLSLRNTFNTAVYHHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVSII
AMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGGGCGTGCCCTGCTTGTACAGGTG
GGAGGCTGGAACATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCATTCCAGGGGAAGGGAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAGCTTTGGAATCAT
GGTGTGATGGAAGGGATTTACTTTTACTGACTCTGTTTTGGGGAAGCTTTTTTGAAGCATT
TCATGCTGAGTCCCTTTTACCTTTGATGTTTGIAAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAAGT
GATTATAACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGTATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTTGGTTGGGCCATGCAGGCTGCTGCCTATAT
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTGGAAGACATGATTGATTACTTTTGTG
ATATTCACGAACCACTTCAACTCCTCATATTCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTACATCCAAG
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACACATTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTCACGTCCACCGGTATCCAATAGACACCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCTTCTATCAAG
GGGAGAGAATTTTTATTTTACCGGACAGAGTGTCAATCCACCTTGCAAGTCTGAACTCAGGGTC
CTTGTGGTCAAATTTGCTCTCTATACTGTATTGGACCTGTTAGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTGCATGACTATGTCGAATATTTCTTACT
GCCATCATTATTTGTAAAGATATTTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTT
TTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

FIGURE 102

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSIFMLSP
 FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM
 FLWNCIMRYSYLREKICLKASLKGVPFGFGWAMQAAAYIFIHRKWDDKSHFEDMIDYFCDIHEP
 LQLLIFPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGTFVVDRLREGKNLDAVHDITVA
 YPHNIPQSEKHLQGDFFPREIHFHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERLRSFYQGEKNF
 YFTGQSVIPPCKSELRVLVVKLLSILYWTLSFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG
 LEIIEIACYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
 TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACAGGAATA
 TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
 CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT
 TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC
 CACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACTGA
 GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAACATCACTCCCTCGG
 ACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTACGATGAGGAGGCCACCTGGGAGCTG
 CGGGTGGCAGACTGGGCTCACTTCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA
 GTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC
 AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
 ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCTATGA
 GGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTA
 TTTTACTCGGGTTACTCTGTGGTGGCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTC
 AAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
 AGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
 TTTCTGATCTGAAAACGTAAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA
 TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
 CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACA
 ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTC
 ACATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT
 GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC
 TGACATGTCAGTTTGAAGGCTTGTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAG
 GGGACTCCCATATTCATATGTCCAGTGTCTGCGGATGAGACAGAGAAGACCCCTGCTTAAAGGGC
 CCCACACCACAGACCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCTCTCT
 CCGGAGCCTGCGCACAGAGAGTACGCCCCCCTCTCCTTTAGGGAGCTGAGGTCTTCTGCCCC
 TGAGCCCTGCAGCAGCGGCAGTCCAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG
 TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATAGGTTTGTGAAAAA
 CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTGCTAGTCACGG
 ACAGTGATTCCTGCCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGACAGTT
 TGAGGGCACAGTGTGCTAATGATGTGTTTTTATATTATACATTTTCCACCATAAACTCTGTT
 TGCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC
 TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTTCACTGATTCTATAAGCCCAGCAT
 TACCTGATACCAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC
 CTCATTAAACACAGACACAAAAATTTAAATAAAATTTTAACAAATTAACATAAACAATATATTTA
 AAGATGATATATACTACTCAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTTAATTTTAAAT
 ATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 104

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVMGMIIVFFK
SKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
 TTTGTTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA
 CTCACTGTTTCATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC
 TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
 CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTC
 AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGA
 AACTGTAGATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
 ATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
 ACACGAAGAAGTAAACTCTAGGTGAGTCTCAGGATCGTTGGTGGGACAGAAAGTAGAAGAGGGTGAATG
 GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
 TTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA
 ATAAAACCTTCGAAAATGAAACGGGCTCTCCGGAGAATAATTTGTCCATGAAAAATACAAACACCCATCACA
 TGACTATGATATTTCTCTGTCAGAGCTTTTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTC
 TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTGTGACAGGATTTGGAGCACTGAAAAAT
 GATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTTGCAATGAACC
 TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
 GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG
 AGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTGTTATACTAGAGTTACGGCCTTGCGGGACTG
 GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTG
 GGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA
 ATAAACTGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
 GATCAACTCTGTATCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
 ATTACAGCCTGTATTCATTTGTTCTCTAGAGTTTTGTGCAATTTTGACTTGTGACATAAATTTGTAAT
 GCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTCAGCTCCTCTCATTTACAGCAAATATCCATTT
 TCAAGGTGCAGAACAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAA
 AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTCAATTATGAAAGGTCAAGCAAAGACA
 GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAGCCAAG
 ATATATCCTTATTTTCATTTCCAAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT
 ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG
 TTAGTGAGGATGTCAACATATAACAATAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDKLY
 AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
 PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
 TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
 RRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
 QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWYLAG
 IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTG
 CCCCAGATGAGCCCCCGCGTCCCGGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCAGC
 GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT
 ACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCCTGTCTACGCCCTCAA
 TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA
 ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCTT
 GTGGTTTCATCCGGTCATGATTGCTGTTTGGCTGTTTCCCTTATCATTGTGGGGATGTTAGGATATTG
 TGGAACGGTGAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGTCTGTCATTTTCT
 GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA
 GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA
 TGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGG
 AAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTTAGAGAATTTCCAGGATGTTCCAAA
 CAGGCCCCACAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATCCCTT
 TTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
 TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAGGGAGCTGGG
 ACAGACCAATGATGTCCTTGAAGAATGACAACCTCTCAGCACCTGTCTATGTCCTCAGTAGAACT
 GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT
 TTGAGATGGAGGAGTTATAAAAGAAATGTACAGAGAAAACCACAACTTGTTTTATTGGACT
 TGTGAATTTTGGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAA
 TAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTC
 ACCACCTGGACAATAATGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
 TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCA
 TCCATGCAACAGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAA
 CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
 CTCAGCGATCTATTCTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT
 ACCTAAATGTGATTTTGTCTGGTTACTAAAATATTCTTACCCTTAAAAGAGCAAGCTAACACAT
 TGTCTTAAGCTGATCAGGGATTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTAGTCGAT
 TTCAGTTCTGATAATGTTAAGAATAACCATATGAAAAGGAAAATTGTCTCTGATAGCATCATT
 ATTTTTAGCCTTTCCGTGTTAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC
 TGTATTTTAAACTTTAACCCTAATTTTGAATAATACCAAGTGTGATACATAGGAATCATTATTC
 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTGAGA
 AAGGACTTGTATGCTGTTTTTCTCCAAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAAA
 GCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTTACAGAAAA
 TAGTGTTCCTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATT
 CTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAATTTTTTTACAA
 GAGTATAGTATATTTTAAATGGGAAAAGTGCATTTTACTGTATTTTGTGATTTTGTGTTTAT
 TTCTCAGAATATGGAAGAAAATTAATGTGTCAATAAATTTTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMDYLNNVLTTLTAETRVEEAVILTYFPVVHP
 VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMT
 LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
 EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPQDQM
 MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP
 TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
 YCGHFYDIEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
 LRSDGKTCEDEVEGCHNNGGCSHSLGSEKGYQCECPRGLVLSEDNHTCQVPEVLCKSNAIEVNIPRELVGG
 LELELTNTSCRGVSNNGTHVNILFSLKTCGTVDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
 CEFPRLYTISEGYVFNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEFPYREALPTLKLRLDSLYFGIEPVVHV
 SGLESLVESCFAPTPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVKGDKHKEVFLHCRV
 LVCGVLDESRCAQCCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
 522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
 GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
 CCTGTGCTGCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGC**ATGT**
 TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAAACCCGTATCCCC
 ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
 GGTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA
 GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
 CCCGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
 AGGGAACCTGGTCTCTGCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
 GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAAACAGCCAG
 GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCAGTGTCTTGCTG
 TGGGAAGAGCCTGAAGACCCCCGTGTGGTGGGTGGGGAGGAGGCTCTGTGGATTCTTGCCCTTGGCAGG
 TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA
 GCCCCTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG
 CTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAAGACAATGACA
 TCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
 GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGAA
 GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGT
 ACCAGGGGGAAGTCACCGAGAAGATGATGTCTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGCT
 GACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
 CTGGGGGGGCCCCAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
 GGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCCTTGCAGTGTCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT
 GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT
 TTCTTGAGAGCAAGAGGGCTCAATTCCTGTAAGAGACCTCGCAGCCAGAGGCGCCAGAGGAAGTCA
 GCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
 CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCC
 CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA
 GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
 ACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA
 AAAA

FIGURE 113

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTCAGCAACTAAAAAGCCACAGGAGT
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC
TGTTTTTGTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACCTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTACCAACTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGACAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTCATAGGCGATGGCTCCCACTGCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCGTGACACCTGCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCCCATCTAACCTTTTCATGTCTGCACATCACCTG
ATCCATGGGCTAATCTGAACCTGTGCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCAATCTCCTGGAACATGAGG
GAACCGCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATTATGGGTGAGAAAAGATG
GAGGTGTTGGGTATCACAAGGCATCGAGTCTCCTGCATTGAGTGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGCTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTGGCCAGGAGGTGAGCAAGGCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTT
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA
AACCTAAGAACCAGGTGCATTAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA
TGTTTATTTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCŞLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:
amino acids 1-15

FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
 AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
 ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAATTGTCCT
 GTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAAGCCTATGACATGGAGCACACTT
 TCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTGACCAGAAGTGAATA
 TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
 CATCTACTTCGTGGGTCTTCAAAAATGTTTATCAAACTCAGATTAAAGTGATTCTGAATTTT
 CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTCTTTGAACAGTCAGTG
 ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA
 GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG
 ACTTTGAGGAGGAGGAGAAGATCTTCACCTTCCTGCCAACGAAAAAAGGGATTGAACAAAAT
 GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGA
 AGAAGTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG
 GTTATTGTTGTATTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
 GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTGTCGTATCATGCCTTG
 TAACTGGTGGGTGGCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC
 TGCTGGCAACATATAATAAATGCTATTCATGAATTTCTGCCTATGAGGCATCTGGCCCT
 GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTCATGTTCTAATAAACTTCTACA
 TTATCACCAAAAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAYDME
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKSKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD
ERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-
242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 117

GAGCTCCCCCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
GGCGGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCCTCCTGTCCATCCTGGGGCT
GGCGGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACTT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTCCGAGCCCTGATGATCGTAGGCATCGTCCT
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTCAATTGCTCTCAGGTCTTTGTGCAATTGCTGGAGTG
TCTGTGTTTGCCAAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGCAGACTGTTAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGGGCTGGGTGCTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCACTACAAA
GCCGTTTCTTATCATGCCCTCAGGCCACAGTGTGGCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCCTT
TGGGTCCAAACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCACGACTATGTGTAAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCACCATAAAACA
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
TTCTCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACTTTGAAGGAAA
GAGTAGACCCAAAGATGTTATTTTCTGCTGTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATA'TTGTAACTCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTG
TTGACATCTTCTTATACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTCTGT
CGCGGGTCAGAAATTGTCCCTAGATGAATGACAAAATATTTTTTTAATTTAAGTCCTAAATATAGTTAA
AATAAATAATGTTTGTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAAATAATGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA
TGGTGGCATAACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAAACTAATCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
 YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
 CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
 CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
 V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGGAGTCC
 AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG
 GTGGTGTGGAAATGGTGGGCACAGTGGCTGTCACTGTCACTGCCTCAGTGGAGAGTGTGGCCCTTCATT
 GAAAAACAACATCGTGGTTTTTTGAAAACCTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
 CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAG
 GACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC
 ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGTGACGGCTGGAATCATCTTCAT
 CATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA
 ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA
 CTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTGCAACGAAAAGAGCAGTAGCTA
 CAGATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG
 TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGCCATGCAAATG
 AAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTACTGTTCTTAACTGCCT
 AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTCAGCAGAATGAGATA
 TTAAACCCAAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
 CTCTTTTTATCATTTACTTCAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC
 ACGACATAGCATTATGTACATAGATGAGTGTAACTTTATATCTCACATAGAGACATGCTTATATGGT
 TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
 ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCA
 TTTATAATGAAGATTAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
 GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT
 CTTGTGTATTAAATTAACATTTTTAAAAACGCAGATATTTGTCAAGGGGCTTTCATTCAAACCTGCTT
 TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
 AAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGAT
 ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA
 TGTCTTGGTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT
 GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTGTCTGTGAAAAATAAATTTCCCTCTTGTA
 CCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTCTGTTTATCCAAATTTGATGAA
 ACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTT
 TATACATTTATATTAATAAATTGTACATTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRMQCK
IYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 121

GGAGAGAGGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG
 CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGAGCC
 GGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCCGAGCGGCTCCGCGGCCTCCTGCTGCTCC
 TGCTGCTGCAGCTGCCCCGCGCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG
 CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
 TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTGCGGATG
 GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCTGGACACCCAACTAC
 AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGATACATT
 TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCACTGGCTCACTTCGGCTAAAATGCA
 GAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTGAGGACCTCTTCCC
 ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG
 CACTTCTTCTGTGAAGGACTTTGTGAAGGAATTGGTGTGGATTAGTGGATGTTGCTATCTGGG
 TTGGCACTTGTTGAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
 ATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCC
 TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
 CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTG
 CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT
 CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTAA
 AAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT
 TAAATAAAAATTATTTCCAACA

Signal peptide:

Transmembrane domain:

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FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
 CTGGGTGCTCATCAGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
 ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATGTAGGATCCAGTTTTTTTTTTA
 ACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC
 TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTATTTGTTCTTGGAG
 TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
 TCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGTGTGTCATGCAACTG
 GCCCCAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
 TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCCACTGTCTTACTGACAATG
 CTTTCTTCTGCGGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA
 ATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
 ATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
 CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTAATGGAATACGCAGACCAAAAGA
 GCTGATTCTTAGTTCCAATAGAATCTCCTATTTCTTAACAATACCTTCAGACCTGTGACAAATT
 TACGGAACCTTGGATCTGTCTTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
 CGGAAGCTGCTGAGTTTACATTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA
 AGACTGCCGCAACCTGGAACCTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
 TCTTTGCTGGCATGATCAGACTCAAAGAACCTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
 CTGGCCCTTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGAATAAAATCAGTGT
 CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGA
 TCGAAGCTTTTCAAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT
 TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG
 TCTTGTGGAATATATGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTGAAAAGTT
 TTAAAGGTCTAAGGGAATACAATTATCTGTGCCAGTCCCAAGAGCTGCAAGGAGTAAATGTG
 ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTATCTGGCCAG
 GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCAAGGCCGAAGCATGAGAGCAAAACCCCTT
 TGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
 TTCCATAAAATCATCGGGGCGAGCTGGCGCTTTTCTGTCCGTGCTCGTCATCTGTGTTAT
 CTACGTGTGATGGAAGCGGTACCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
 GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCAGGAATTTTATGTA
 GATTATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCTGCACCTA
 TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAAGCT
 GGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCTCCCC
 TTCCCTCTCCCTCTCACTTTGGTGGAAGATCCTTCTTGTCCGTTTTAGTGCATTACATAACT
 GGTCAATTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT
 GAACCTCCGTTTAAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCAATTT
 GTTTTAAGATAAACTTCTTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPKGCRCGKMVYCESQKLQEIPSSISAGCLG
LSLRYSNLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDSLQNQLHSLGSEQFRGLRKLLSLHLRSNSLRITPVRIQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTMSWTWSSLQRLDL
SGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADAEHISFHKIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRRHRKKKRQSLQMTPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCGGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG
 ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT
 AGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAATGCAAGGAGAAGCAGCTCTTGCTC
 GGTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
 ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
 GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAGTGAAG
 ATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT
 TTAGCCAATCCAACGACCTAGTGAAGGTTTCAGATGCAAATGGAAGGAAAAGGAAACTGGAAGG
 AAAACCATTGCGATTTCGTGGTGTACATCATGCATTTCGAAAAATCTTAGCTGAAGGAGGAATAC
 GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA
 ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC
 TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
 TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG
 ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC
 ATCTTGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGA
 TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMOMEGKRRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIXSRIMNQP
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 128

MARPGMERWRDRLALVTGASGGIGA A VARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALSICTR
EAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQTHIRATC
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:**Signal peptide:**

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AACCTCTACATGGGCCTCCTGCTGCTGGTGTCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
 CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGGGAGC
 ACCTCCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCAGTTCTGGTTTCATGC
 CAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
 GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTTTCAGTAGCCACCAGCCACCTGTGG
 CCGTTGAGTGCTTGAAATTGAGGAAGTGAAGAAATTAATTTCTCATGTATTTTTCTCATTATTTA
 TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
 TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT
 TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
 CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCAAGTAGCTGGGACTACAGGCAT
 GCACCACAATGCCCAACTAATTTTTGTATTTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG
 CTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCTCGGCCTCCCAAAGTGTTATGATTACA
 GGCGTGAGCCACCGTGCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGGAAGTTTGAAATTAT
 ACAATGAATTATTGTTAACTGTCTCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
 ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
 AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG
 AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG
 TTCCATCCATGTTGCTGCAAATGACAGGATTCGTTCTTAATTTCAATTAAATAACCACACATG
 GCAAAAA

FIGURE 130

MGLLLLVLFSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGHGTLGESPMFPKRVCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
 ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
 TCCATCTGTGTGCGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTTCTGACATCCATTCCAACAG
 GAATACCAAGAGGATGCTACAACCTCTTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCCTCAGAT
 TTGAAAACTTGCTGAAAGTAGAAGAATATACCTATACCACAACAGTTTAGATGAATTTCTACCAACCT
 CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCATTATGATTCACTTTCAA
 AAATTCCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
 TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAAATCCCTGGGGTTT
 GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTCATCACCATCTCTTCAAG
 GTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT
 TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATCCCTGACTGCTGCACCAGTAAACCT
 TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTCCCCCAATGCTTTT
 CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGTATCTTT
 GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
 GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
 AGGTTTCGTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTGATTGTAAGGACAGTGGGATTGTAAGC
 ACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCCAAGGACAGTGGCCAGCTCCAGTGAC
 CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA
 CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCATATCTCTTGAAACTTGCTCTACCTATG
 ACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT
 AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCCATATAAAGTATGCATGGTTC
 CCATGGAAACCAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT
 CGAATGTACAACCCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC
 TTTGGCTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATGCCCCTTCTTGCTTTAGTGTGTGGTATG
 TTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
 GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTTCTTTTCAGATGTTACCAAT
 AAGCAATGAACCCATCTCGAAGGAGGAGTTTCTAATACACACCATATTTCCCTCCTAATGGAATGAATCTGT
 ACAAAAACAATCACAGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC
 TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG
 GT

FIGURE 132

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCNDRFLT SIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTTITYDSLSKIPYL
EELHLDNDSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRQLYRLDMSNNLSNLPQGIFDDL DNITQLILRNNPWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGGWPAPVTKQPD
IKNPKLTKDQQTGSPSRKTTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET
IVTGERSEYLVTALEPDSPYKVMVPMETSNLYLFDETPVC IETETAPLRMYNPTTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSNRSYRDSGIPDS DSHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCCTTCCCAGAGTCCTTTGCCCAGGCCACCCAGGCTTCTTGGA
 GCCCTGCCGGGCCACTTGTCTTCATGTCGTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
 TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG
 GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT
 CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
 GCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
 GGGGCTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGAGAAGTGGGCCAGGAGCCCTGC
 TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
 CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCTCCAGCCCGG
 GTTTTGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACAGTTCGGGC
 CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG
 GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC
 AGGCTACTGCCTGTCCACCACTGCTCTTCTCTCTGCGCCAGAATGAGGGGATGCACACAGG
 GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
 AGAGCTGAGGCCATCGGATACGCCTACCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG
 TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
 AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
 TATCAGCAGCATTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT
 TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCGAAGC
 AATTCTCTTGCTCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT
 TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAATCCTGAT
 CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTTGGGATTATAGGTGTGAGCCACCGTGTCTG
 GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
 ATGGGGGCTCTCTCCCTTAGATGGCTGCTCCTCCCAACACAGCCACAGCACTGGCAGCCCTGG
 GTGGCTTCTATACATCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG
 CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
 TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
 ATAAGCAAAGCCACCCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
 GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

FIGURE 134

MSARGRWEGGRRACRGSGLARAQGAERVTSSEQRPAMASLGLLLLLLLLTALPPLWSSSLPGLD
 TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRLVEEQKSVREKWAQEPLLOPLSLRV
 GMLGEKLEAAIQRSYLHLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE
 RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQSQD
 YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSQKQEGCFG
 EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSLILP
 SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGAGTTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGCGGGCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACGTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCACCTGAATTAATTACAGTGTCCTATAGAAAATGCCATTAATAAATTAT
ATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF
SSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 139

CCTGGAGCCGGAAGCGGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCAGCC
TAGCGTGTCCACGATGCGGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC
TAGGGATCGCGGTCTTCCCTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCCAGAGCGGAA
CACGAGCGGAGCCCCAGCGCCGAACCCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC
ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTTG
GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGGAAAAAGGAGCATCTCACAGT
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG
CCTTCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGA
TAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA
TTCCCAAAGCATTGTGGAATATGATGGAACAACCTCATTTTTCGTGTCAGATTACACAGAGGT
GGATAATAATGTCACGAGGCATTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAAATCC
TCCACTACCTGGGGCTGGACCACATTGGCCACATTTCAGGGCCCAACAGCCCCCTGATTGGGCGAG
AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCCGAAGGAGAGAGA
GACGCCCTTACCCAAATTTGCTGGTTCTTTGTGGTGACCATGCGATGTCTGAAACAGGAAGTCACG
GGGCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAGGAAA
CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGGCAGACTGGCGATAGC
ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGAC
CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAACTGTTGCAAGAG
AATGTGCCGTCATATGAAAAAGATCCTGGGTTTGAAGCAGTTTAAATGTCAGAAAGATTGCATGG
GAAGTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAGTCCCTATTCAACCTGGGCTCCAAGG
TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG
TTCTCACCCCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA
CTGTATCTCCTGGGTTTTCTCTGCTCTTTTATTGGTGATCCTGGTTCTTTTCGGCCGTTACGCT
CATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCTCTCGTGGCTGGCGGCAGGCT
GCCTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGGCTGGAC
AGGGGGCTCAGGGAAGGACGTGGAGCAGCCTATCCCAGGCTCTGGGTGTCCGACACAGGTG
TTCACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGGAAAGCTAGGTTCTGCGACTGTTAC
CAAGGTGATTGTAAAGAGCTGGCGGTCACAGAGGAACAAGCCCCCAGCTGAGGGGTGTGTGAA
TCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCTGGA
CACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCCTGCCACCCCCAGAATGCATCCT
GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTTGGAATTTAGTCCCTGGCC
TCGGACACCTTCATTGCTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC
ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCC
ACCCCAACCTGCACAGCCCTCATCCCTCTTGGCTTGAAGCGTCAGAGGCCCTGTGCTGAGTGT
CTGACCGAGACACTCACAGCTTTGTATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTG
CCACGCTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG
CTGCACACAGTATGTAGTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWWKLFPKHFVEYDGTTSFFVSDYTEVDNNV
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTACTGCTGCTGTTGGAGTACAAC
TCCCTATAGAAAACAAC TGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTCAGCATTTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCCAGATAAAAAC TACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAACTAATTGTATAAAAAACCAAACCTGCTCACT

FIGURE 142

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLD SGNLI AVDPKNYIRPEI
 FFALASSLSSASA EKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI
 FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA
TCCAGGATCCTGTCCCTTCCTGTCTGTAGGAGTGCTGTTGCCAGTGTGGGGTGAGACAAGTTTG
TCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTGTGGG
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACTGCCATTTCOAAGAAAGCACAG
AGCTGAACAATACTTTCACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTGAGTGAAACCCACTCACAGGCTTGTCATGT
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT
TTGGACTTGTTTGTATCTATTTTGCATGTGTTTGAATCTCAGATCAGTGTTTTAGAAAATCC
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAA
AAA

FIGURE 144

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLEGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCCATGAGGAAG
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA
GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCAGCACTGCCCAGATCA
CTGAGGCCCAGGTGGCTGAGAACC GCCCGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTTTAGAGGTAG
GTGTATTCCCGTTTTACAGATAAGGAAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSSWWLATVCMLLFSLHSAVQTRGIKHKRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMLVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 147

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATTT
 CCTGATGATTTATAGACTCAAAGAAAACTATGTTCAGAAGCTCTCTTCTTCTTGGCCTCCTCT
 CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG
 AAATCTTTCATTTTGCTTGTGAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTTTGAAATTT
 CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATTGATGCTGAGG
 TTTGGGGT

FIGURE 148

MFRSSLLFWPPLCLLSLFLILLISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 149

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGACTTGAC
TCCCGCGCGCCCCAACCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC
CGGCCCCCTCTCCCGCCCCACCCACCTCCTGGCTCTTCTGTTTTACTCCTCCTTTTCATTGATA
ACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT
CCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCCCGATTCAAGCTTTCCCCAAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTT
TGTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAAGT
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCAACTAGACGGGACTCCTTTAACCCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACA
TTATGAGGAGGATCCCAATAAGCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGACAACCTTTGAGGAAGTCCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAAGAACAAAAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGAAAAGGAATATGGAAGCTTGAAGGATTCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTTGAATGGTTGAAGAAACATGACAAAAAGGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAAAATGGCAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAATTTTTTGACCAAGG
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTAAAAACATAGCTTTCTTCCC
GTAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCTGTGGAGCTCAA
GATGTGCTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
 ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
 GTGGTCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCGTCATCCTGGGTGTCCAGGGTGAAG
 CCAGTGCCTGTCATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
 AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTACCTTCTACCGGGGACATGGGGCTCACC
 TCCAGCTTCGAGTGGCTGCCTACCGGGGTGGTTCCTGTGCAGGTGCCTGAAGCCGATCAGCC
 TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCC
 AGCAGTGTGACTAGGGCAACGTGCCCCCAGAAGTCCCTGGGCAGAGCCAGTCTGGGTGAGGGGT
 GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGCTCTCAGGACCCCAAGTCTGACTTAG
 TGGGCACCTGACCCTTTGTCTTCTGGTTCCCAGTTTGGATAAATTCTGAGATTTGGAGCTCAGT
 CCACGGTCTCCCCACTGGATGGTGCTACTGCTGTGGAACCTTGTA AAAACCATGTGGGGTAAA
 CTGGGAATAACATGAAAAGATTCTGTGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGCT
 TAATGGTAACGTGACAAGTGTTACCTGAGCCCCGAGGCCAAGCCATCCCCAGTTGAGCCTTATA
 GGGTCAGTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
 GAGTCAGGGATCTATGCCCCCTGGCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTGATA
 TGCTACCTTTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTATGTCAGAA
 GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTAAAAACCCAA
 GATACAAATCAAAATCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGTCTATGACATATTGAGA
 AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATACCTATTTATATATT
 TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGTGGTGGCAGTAT
 AGGTGATTTTTCTTTAATTCTGTTAATTTATCTGTATTTCTTAATTTTCTACAATGAAGATGA
 ATTCTTGTATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
 TTGTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
 TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTGT
 GTGGCTGGAATCTCTGGGTAAAGAACTTAAAGAACAAAAATCATCTGGTAATCTTTCTTAGAAG
 GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAAGCTGTGTACTGGTTGA
 ATTGTGTCCTCCCTCAAATTCACATCCTTCTTGGAACTCTCAGTCTGTGAGTTTATTTGGAGATAAG
 GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCTGCTGGATGAAGGTAGACCTAAATTCATAT
 GACTGGTTTCCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
 AAGATGAAGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
 ATCAGAAGCTTGGAAGAGGCAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
 CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGATAAATTTCCGCTGTTTTAA
 GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT
 CTCCTCGTGTTTACATTCTGTGTGTGTCCCCCTCCCAATGTACCAAAGTTGTCTTTGTGACCAA
 TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC
 TACTTGAGCCCTCTCTCTGCCCCACCGCCCCCAATCTATCTTGGCTCAGTCTGCTGGGGG
 AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT
 GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
 AAGTTGCTCAGTTTTGGTCTAACTTGTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILGVQGG
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
VRLTQLPENGGWNAPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTCTGCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACTTCACCCCTGAAGAAGTGTGTTCCCTCAATCTGATAGGTTT
CAGCCTTATATGCAGGAGGTGGTGGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGTGGATTGTCTGTTTATGTCTCTGAGAAAT
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACCAAAGGAAGATGGGAAGCCAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGTATTTATTATTATTATAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 154

MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRDKNFQQPYITNRTFMLAKEASL
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLARLSNRLS
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT
 CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCAGCATGTACCAGGTCAGTGCAGAGGGC
 TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC
 TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCGAGAT
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCTACAGGTGGTTCAT
 TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGG
 CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG
 GCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT
 CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCCGT
 TGCCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA
 GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA
 AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTTCCTTAGCTTGTGTGTGTGTGCGGGCCCGT
 GTGATGGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA
 ACCACTTGCCATGAAGGGCCAGGATGCCCAGATGCTTGGCCCCCTGTGAAGTGCTGTCTGGAGCAG
 CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACCTTCTGCACATTTTGAAAAGAG
 CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTTCAAA
 GTTCTGCCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTCCCATCCCCTGCTACCCCTG
 GCCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCTGGTTTTATT
 TGTTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT
 TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT
 CTTTATTTAAAAATGAAAAA

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA
 RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
 ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCGAGAGCC
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAA
GATTTGTGTGACGGGCAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTATTGGGGCCCATATATTCCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGATGAGGAGACA
GTAGAAGTGAACCTCACAACCACTCCCCGAGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTCTCAGGTGTTTGTAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGAAGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCGAGAAGTGAGGTGCATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGTCTTCTTCTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTTAACCTTTTCTGCA
GTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSFEWMLQHDLPGLRDLRVEPVTTSVATGDYSILMNVS
 LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
 NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH
 STIIGFSQVFEPHOKKQTRASVVIPTVDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK
 SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTLLPPIKVLVVPSEICFHHTICYFTEFL
 QNHCRSEVILEKWQKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSFSENSQDLFPLA
 FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCCKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD
 GCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283
 - 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
 GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
 CTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
 ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
 GAATTACACTGTCACCTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGA
 ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCGGTTCCTATCCAGCAA
 GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTCTTTCCAGTTGGAGAAGGTGCT
 GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC
 ACTCAGCTGAAGAAG

FIGURE 16o

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVSMERNIESRSTSPWNYTWTWDPNRYPSSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVV
RRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

FIGURE 161

A C A C T G G C C A A A C A A A A A C G A A A G C A C T C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C C C A G G
 A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C T C T G G A G G C T G A A G A G G G A T T C
 C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C C T T G G G G G G G G C A G C A C
 A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G A T G C C T G T G C C C T G G T T C T T G C T G T C C T
 T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G G C T T G T G G G G C C T C A G G A C G C T A C C
 C A C T G C T C T C C G G G C C T C T C C T G C C G C C T C T G G G A C A G T G A C A T A C T C T G C C T G C C T G G G G A C A T
 C G T G C C T G C T C C G G G C C C C G T G C T G G C G C C T A C G C A C C T G C A G A C A G A G C T G G T G C T G A G G T G C C
 A G A A G G A G A C C G A C T G T G A C C T C T G T C T G C G T G T G G C T G T C C A C T T G G C C G T G C A T G G G C A C T G G
 G A A G A G C C T G A A G A T G A G G A A A G T T T G G A G G A G C A G C T G A C T C A G G G G T G G A G G A G C C T A G G A A
 T G C C T C T C T C C A G G C C C A A G T C G T G C T C T C C T T C C A G G C C T A C C C T A C T G C C C G T G C G T C C T G C
 T G G A G G T G C A A G T G C C T G C T G C C C T T G T G C A G T T T G G T C A G T C T G T G G G C T C T G T G G T A T A T G A C
 T G C T T C G A G G C T G C C C T A G G G A G T G A G G T A C G A A T C T G G T C C T A T A C T C A G C C C A G G T A C G A G A A
 G G A A C T C A A C C A C A C A C A G C A G C T G C C T G C C C T G C C C T G G C T C A A C G T G T C A G C A G A T G G T G A C A
 A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A C T T C G G C C T C T C C C T G T A C T G G A A T C A G
 G T C C A G G G C C C C C A A A A C C C C G G T G G C A C A A A A A C C T G A C T G G A C C G C A G A T C A T T A C C T T G A A
 C C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A G G T G T G G C C T C T G G A A C C T G A C T C C G T T A G G A
 C G A A C A T C T G C C C C T T C A G G G A G G A C C C C G C G C A C A C C A G A A C C T C T G G C A A G C C G C C C G A C T G
 C G A C T G C T G A C C C T G C A G A G C T G G C T G C T G G A C G C A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T
 G T G C T G G C G G G C T C C G G G T G G G G A C C C C T G C C A G C C A C T G G T C C C A C C G C T T C C T G G G A G A A C G
 T C A C T G T G G A C A A G G T T C T C G A G T T C C C A T T G C T G A A A G G C C A C C C T A A C C T C T G T G T T C A G G T G
 A A C A G C T C G G A G A A G C T G C A G C T G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T C A A G A
 C G A T G T G C T A C T G T T G G A G A C A C G A G G C C C C A G G A C A A C A G A T C C C T C T G T G C C T T G G A A C C C A
 G T G G C T G T A C T T C A C T A C C C A G C A A A G C C T C C A C G A G G G C A G C T C G C C T T G G A G A G T A C T T A C T A
 C A A G A C C T G C A G T C A G G C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G
 C C C C A T G G A C A A A T A C A T C C A C A A G C G C T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T T G C C G
 C T G C G C T T T C C C T C A T C C T C C T T C T C A A A A A G G A T C A C G C G A A A G G G T G G C T G A G G C T C T T G A A A
 C A G G A C G T C C G C T C G G G G C G G C C G C C A G G G G C G C G C G G C T G C T C C T C T A C T C A G C C G A T G A
 C T C G G G T T T C G A G C C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G C C A G C T G C C G C T G C G C G T G G
 C C G T A G A C C T G T G G A G C C G T C G T G A A C T G A G C G C G C A G G G G C C G T G G C T T G G T T T C A C G C G C A G
 C G G C G C C A G A C C C T G C A G G A G G G C G G C G T G G T G G T C T T G C T C T C T C C C G T G C G G T G G C G C T
 G T G C A G C G A G T G G C T A C A G G A T G G G G T G T C C G G G C C C G G G G C G C A C G C C C G C A C G A C G C C T T C C
 G C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G C A G G G C C G G G C G C C C G C A G C T A C G T G G G G
 G C C T G C T T C G A C A G G C T G C T C C A C C C G A C G C C G T A C C C G C C C T T T C C G C A C C G T G C C C G T C T T
 C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C C G C G T T C C G
 G G C G G C T C C A A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G C T A C T T C
 C A T C C C C G G G G A C T C C C G C G C C G G A C G C G G G T G G G A C C A G G G G C G G A C C T G G G G C G G G G A
 C G G G A C T T A A A T A A A G G C A G A C G C T G T T T T T C T A A A A A A

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT
GCTCACGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA
AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTACGCGGATCACCCGGAAGTCTGCTG
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
GTCAGTGCGGGAGGCGGTGAGCCACCAAGATGACTGACAGGTTGAGTCTCTGACGACACTAC
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGTATTGTTTCATCCTA
CCCCACGCCAATCCGTGACGGGATGGCCACCGGCTAACCTGGAAGACATCTTCCATGACCTG
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGAGGGGAAGCAGAGAGA
ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTTGCGTTCCCA
CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCGGAGTGAAGACACTGCCAGACCGGACATGGACC
TACTCCTTCTCCGGAGCCTTCTGTTCTCCATGGGCTTCTCGTCGAGTACTCTGCTACCTGAG
CTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTT
TCCAGCGCTGCGCTTTCATCCAGGAGCACGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC
AGTCTGGCCCAGCCTGTCCAGTACTCCCAGATCAGGGTGTCTGGACCCAGGGAGCCCCGAGGAGC
TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCTCCAGC
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCCAAACGCTGCCCTGAG
GTGCGGCCCCCATCCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTTCTAGCCCCACA
GGCCATCTCTAAGGTCCAGCCTTCTCTATGCCCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT
CCTATGGGGTATGCATGGAAGGTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTTAA
CACCTTAGGCCTAAAGGTGAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT
TTCTCTGCAGGAGGTGACCTTCTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGACCCAGC
CCCTGGGGATTTGCACAGACAGAACATCTGACCCAAATGTGTACACAGTGGGGAGGAAGGGACA
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC
CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCCGTGAGACCTCAGACCTG
GAGCAGCCCCACAGAAGTGGATTCTCTTTTCAGAGGCTGGCCCTGACTGTGCAGTGGGAGTCTG
AGGGGAATGGGAAGGCTTGGTGTCTCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
ATCCCATGCGCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA
AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGTCTGCTGAGCCCTG
CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAAACTCCCGAGGTCCAGAGCCCCACCTC
CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCTCTCCTTGCCCCATTCTTGCCAGTTTC
ACAATCTAGCTCGACAGAGCATGAGGCCCCCTGCCTCTTCTGTCTATTGTTCAAAGGTGGGAAGAGA
GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAACAACTGC
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA
TTCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTGAGCTTCATTCTCTGATAGAACAAAGC
GAAATGCAGGTCCACCAGGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCT
ATCCTGAGAATGGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCCCTGGACGGGTACAATAACACAG
TGTACTGATGTACAACTTTGCAAGCTCTGCCTTGGGTTGAGCCCATCTGGGCTCAAATTCAGC
CTCACCCTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCTCTC
ATCTGTAATGTGGGGATCATAACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAACGGTAGCTATTTAAAAA
AAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDGPEGTPDVTYSIEYKTYGERDW
 VAKKGCQRITRKSCNLTVETGNLTLEYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTICIS
 KVRSIQMIHVPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRITYQMHLGGKQREYEFFGLTPDT
 EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRVTKPPAP
 PNSLVQRVLTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
 YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPSPSYAPQVTPEAQFPFYAPQAISKVQPSSY
 APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSLAM
 EESQEAKSLHQPLGICTDRTSDPNVLHSGEETPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC
 SPSPDQGPSPWGLLESIVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTVQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGGGTGGCCACAACATGG
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACTTTGGGCTGGA
AGTGTGAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAACTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA
ACTTGACCCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTGAGAGGATGGAGAAGGTGCTTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCGCACGATAA
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCTGAAAACAGAAATGAGTCAGAGAGGAAGTGACAGTGCCTTATT
CATTACAGCAAAGGATTTTCGTTGGCATCAAAATCTAAGTTTGTTTTACAAAGATTGTTTTTTAGTA
CTAAGCTGCCTTGGCAGTTTGCAATTTTGTAGCCAAACAAAAATATATTATTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFLGALWWVPGQSDLSHGRRFSDLKVCGDEECMSMLMYRGKALEDFTGPD CRFVN
 FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPAETDFVCFEGGRD
 DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRA DSEGE GA
 FSESTEGLQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER
 EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNL SLYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAGCGC
 AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAAGTTC
 AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG
 CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGGGGCTCGGGC
 GCGGGGAGTAGGGCCCGGCAGGGAGGAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG
 GGCAGAGGCCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG
 TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCGCGCTGGTCAGC
 GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAAGT
 GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCCCTCCTCA
 GCCTTGAGAATGAAGCAGAACAGAAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
 ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAACATCTGG
 TGCCTGCCCAGATCTCTACCAGTGGTCTGATGGAAGCAATCCCAGTACCGAAACTGGTACACAG
 ATGAACCTTCCTGCGGAAGTGAAAAGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGC
 CTTGGGGGTCCCTACCTTTACCAGTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTG
 CAAGTATGAACCAGAGATTAATCCAACAGCCCCGTAGAAAAGCCTTATCTTACAAATCAACCAG
 GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT
 ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTGTTTCCAGATGCT
 GCATAAAAGTAAAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTA
 CCAGAAAAGAAAGTGGCATGGAAGTAAATAACTCATTGACTTGGTTCCAGAATTTTGTAAATTCT
 GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGC
 AAGATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTCA
 TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA
 ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
 TGTGTGTTAGAAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTAGTCAATGTAA
 TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA
 ATGAACTGTTCTAATATTTATTTTTATGGCATCTCATTTTTCAATACATGCTCTTTTGATTAAAG
 AAACCTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT
 TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGA
 AATAAGAAGCTATTTTATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
 TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTGTAGCTTAAATTAACAGATT
 TTGTAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
 TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA
 GGGTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTGGGGTTTGGG
 ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
 ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
 ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAAATGGGTTGG
 AACCCTCAGTGATCGCATATTCATTGATGAGGGTTGCTTGAGATAGAAAATGGTGGCTCCTTT
 CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAAGTCT
 CTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTGTCTTCTGGGGGAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFRCRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRRTKTSNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217